



IFW16

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/798,923A

DATE: 08/27/2004
 TIME: 11:17:34

Input Set : A:\ISIS0124-100 (RTS0739) SEQ(rev).txt
 Output Set: N:\CRF4\08272004\J798923A.raw

3 <110> APPLICANT: Kenneth W. Dobie
 4 Susan M. Freier
 6 <120> TITLE OF INVENTION: MODULATION OF ACE2 EXPRESSION
 8 <130> FILE REFERENCE: RTS-0739US
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/798,923A
 C--> 10 <141> CURRENT FILING DATE: 2004-03-10
 10 <160> NUMBER OF SEQ ID NOS: 152
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 20
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Artificial Sequence
 18 <220> FEATURE:
 20 <223> OTHER INFORMATION: Antisense compound
 22 <400> SEQUENCE: 1
 23 tccgtcatcg ctccctcagg 20
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 28 <212> TYPE: DNA
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 33 <223> OTHER INFORMATION: Antisense compound
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 41 <212> TYPE: DNA
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 52 <210> SEQ ID NO: 4
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 54 <212> TYPE: DNA
 55 <213> ORGANISM: H. sapiens
 57 <220> FEATURE:
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 60 <221> NAME/KEY: CDS
 61 <222> LOCATION: (104) . . . (2521)
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 66 gggaaagtca ttcagtggat gtgatcttgg ctcacagggg acg atg tca agc tct 115
 67 Met Ser Ser Ser



20

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20

60

115

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68	1	
70 tcc tgg ctc ctt ctc agc ctt gtt gct gta act gct gct cag tcc acc		163
71 Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Ala Ala Gln Ser Thr		
72 5 10 15 20		
74 att gag gaa cag gcc aag aca ttt ttg gac aag ttt aac cac gaa gcc		211
75 Ile Glu Glu Gln Ala Lys Thr Phe Leu Asp Lys Phe Asn His Glu Ala		
76 25 30 35		
78 gaa gac ctg ttc tat caa agt tca ctt gct tct tgg aat tat aac acc		259
79 Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr		
80 40 45 50		
82 aat att act gaa gag aat gtc caa aac atg aat aat gct ggg gac aaa		307
83 Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn Ala Gly Asp Lys		
84 55 60 65		
86 tgg tct gcc ttt tta aag gaa cag tcc aca ctt gcc caa atg tat cca		355
87 Trp Ser Ala Phe Leu Lys Glu Gln Ser Thr Leu Ala Gln Met Tyr Pro		
88 70 75 80		
90 cta caa gaa att cag aat ctc aca gtc aag ctt cag ctg cag gct ctt		403
91 Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln Leu Gln Ala Leu		
92 85 90 95 100		
94 cag caa aat ggg tct tca gtg ctc tca gaa gac aag agc aaa cgg ttg		451
95 Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys Ser Lys Arg Leu		
96 105 110 115		
98 aac aca att cta aat aca atg agc acc atc tac agt act gga aaa gtt		499
99 Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser Thr Gly Lys Val		
100 120 125 130		
102 tgt aac cca gat aat cca caa gaa tgc tta tta ctt gaa cca ggt ttg		547
103 Cys Asn Pro Asp Asn Pro Gln Glu Cys Leu Leu Leu Glu Pro Gly Leu		
104 135 140 145		
106 aat gaa ata atg gca aac agt tta gac tac aat gag agg ctc tgg gct		595
107 Asn Glu Ile Met Ala Asn Ser Leu Asp Tyr Asn Glu Arg Leu Trp Ala		
108 150 155 160		
110 tgg gaa agc tgg aga tct gag gtc ggc aag cag ctg agg cca tta tat		643
111 Trp Glu Ser Trp Arg Ser Glu Val Gly Lys Gln Leu Arg Pro Leu Tyr		
112 165 170 175 180		
114 gaa gag tat gtg gtc ttg aaa aat gag atg gca aga gca aat cat tat		691
115 Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg Ala Asn His Tyr		
116 185 190 195		
118 gag gac tat ggg gat tat tgg aga gga gac tat gaa gta aat ggg gta		739
119 Glu Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu Val Asn Gly Val		
120 200 205 210		
122 gat ggc tat gac tac agc cgc ggc cag ttg att gaa gat gtg gaa cat		787
123 Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Glu Asp Val Glu His		
124 215 220 225		
126 acc ttt gaa gag att aaa cca tta tat gaa cat ctt cat gcc tat gtg		835
127 Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu His Ala Tyr Val		
128 230 235 240		
130 agg gca aag ttg atg aat gcc tat cct tcc tat atc agt cca att gga		883.
131 Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile Ser Pro Ile Gly		
132 245 250 255 260		

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134	tgc	ctc	cct	gct	cat	ttg	ctt	ggg	gat	atg	tgg	ggg	aga	ttt	tgg	aca	931
135	Cys	Leu	Pro	Ala	His	Leu	Leu	Gly	Asp	Met	Trp	Gly	Arg	Phe	Trp	Thr	
136										265					270	275	
138	aat	ctg	tac	tct	ttg	aca	gtt	ccc	ttt	gga	cag	aaa	cca	aac	ata	gat	979
139	Asn	Leu	Tyr	Ser	Leu	Thr	Val	Pro	Phe	Gly	Gln	Lys	Pro	Asn	Ile	Asp	
140										280					285	290	
142	gtt	act	gat	gca	atg	gtg	gac	cag	gcc	tgg	gat	gca	cag	aga	ata	ttc	1027
143	Val	Thr	Asp	Ala	Met	Val	Asp	Gln	Ala	Trp	Asp	Ala	Gln	Arg	Ile	Phe	
144										295					300	305	
146	aag	gag	gcc	gag	aag	ttc	ttt	gta	tct	gtt	ggt	ctt	cct	aat	atg	act	1075
147	Lys	Glu	Ala	Glu	Lys	Phe	Phe	Val	Ser	Val	Gly	Leu	Pro	Asn	Met	Thr	
148										310					315	320	
150	caa	gga	ttc	tgg	gaa	aat	tcc	atg	cta	acg	gac	cca	gga	aat	gtt	cag	1123
151	Gln	Gly	Phe	Trp	Glu	Asn	Ser	Met	Leu	Thr	Asp	Pro	Gly	Asn	Val	Gln	
152	325									330					335	340	
154	aaa	gca	gtc	tgc	cat	ccc	aca	gct	tgg	gac	ctg	ggg	aag	ggc	gac	ttc	1171
155	Lys	Ala	Val	Cys	His	Pro	Thr	Ala	Trp	Asp	Leu	Gly	Lys	Gly	Asp	Phe	
156										345					350	355	
158	agg	atc	ctt	atg	tgc	aca	aag	gtg	aca	atg	gac	gac	ttc	ctg	aca	gct	1219
159	Arg	Ile	Leu	Met	Cys	Thr	Lys	Val	Thr	Met	Asp	Asp	Phe	Leu	Thr	Ala	
160										360					365	370	
162	cat	cat	gag	atg	ggg	cat	atc	cag	tat	gtt	atg	gca	tat	gct	gca	caa	1267
163	His	His	Glu	Met	Gly	His	Ile	Gln	Tyr	Asp	Met	Ala	Tyr	Ala	Ala	Gln	
164										375					380	385	
166	cct	ttt	ctg	cta	aga	aat	gga	gct	aat	gaa	gga	ttc	cat	gaa	gct	gtt	1315
167	Pro	Phe	Leu	Leu	Arg	Asn	Gly	Ala	Asn	Glu	Gly	Phe	His	Glu	Ala	Val	
168										390					395	400	
170	ggg	gaa	atc	atg	tca	ttt	tct	gca	gcc	aca	cct	aag	cat	tta	aaa	tcc	1363
171	Gly	Glu	Ile	Met	Ser	Leu	Ser	Ala	Ala	Thr	Pro	Lys	His	Leu	Lys	Ser	
172	405									410					415	420	
174	att	ggt	ctt	ctg	tca	ccc	gat	ttt	caa	gaa	gac	aat	gaa	aca	gaa	ata	1411
175	Ile	Gly	Leu	Leu	Ser	Pro	Asp	Phe	Gln	Glu	Asp	Asn	Glu	Thr	Glu	Ile	
176										425					430	435	
178	aac	ttc	ctg	ctc	aaa	caa	gca	ctc	acg	att	gtt	ggg	act	ctg	cca	ttt	1459
179	Asn	Phe	Leu	Leu	Lys	Gln	Ala	Leu	Thr	Ile	Val	Gly	Thr	Leu	Pro	Phe	
180										440					445	450	
182	act	tac	atg	tta	gag	aag	tgg	agg	tgg	atg	gtc	ttt	aaa	ggg	gaa	att	1507
183	Thr	Tyr	Met	Leu	Glu	Lys	Trp	Arg	Trp	Met	Val	Phe	Lys	Gly	Glu	Ile	
184										455					460	465	
186	ccc	aaa	gac	cag	tgg	atg	aaa	aag	tgg	tgg	gag	atg	aag	cga	gag	ata	1555
187	Pro	Lys	Asp	Gln	Trp	Met	Lys	Lys	Trp	Trp	Glu	Met	Lys	Arg	Glu	Ile	
188										470					475	480	
190	gtt	ggg	gtg	gtg	gaa	cct	gtg	ccc	cat	gat	gaa	aca	tac	tgt	gac	ccc	1603
191	Val	Gly	Val	Val	Glu	Pro	Val	Pro	His	Asp	Glu	Thr	Tyr	Cys	Asp	Pro	
192	485									490					495	500	
194	gca	tct	ctg	ttc	cat	gtt	tct	aat	gat	tac	tca	ttc	att	cga	tat	tac	1651
195	Ala	Ser	Leu	Phe	His	Val	Ser	Asn	Asp	Tyr	Ser	Phe	Ile	Arg	Tyr	Tyr	
196										505					510	515	
198	aca	agg	acc	ctt	tac	caa	ttc	cag	ttt	caa	gaa	gca	ctt	tgt	caa	gca	1699

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199	Thr	Arg	Thr	Leu	Tyr	Gln	Phe	Gln	Phe	Gln	Glu	Ala	Leu	Cys	Gln	Ala
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202	gct	aaa	cat	gaa	ggc	cct	ctg	cac	aaa	tgt	gac	atc	tca	aac	tct	aca
203	Ala	Lys	His	Glu	Gly	Pro	Leu	His	Lys	Cys	Asp	Ile	Ser	Asn	Ser	Thr
204		535					540				545					
206	gaa	gct	gga	cag	aaa	ctg	ttc	aat	atg	ctg	agg	ctt	gga	aaa	tca	gaa
207	Glu	Ala	Gly	Gln	Lys	Leu	Phe	Asn	Met	Leu	Arg	Leu	Gly	Lys	Ser	Glu
208		550				555			560							
210	ccc	tgg	acc	cta	gca	ttg	gaa	aat	gtt	gta	gga	gca	aag	aac	atg	aat
211	Pro	Trp	Thr	Leu	Ala	Leu	Glu	Asn	Val	Val	Gly	Ala	Lys	Asn	Met	Asn
212	565				570				575			580				
214	gta	agg	cca	ctg	ctc	aac	tac	ttt	gag	ccc	tta	ttt	acc	tgg	ctg	aaa
215	Val	Arg	Pro	Leu	Leu	Asn	Tyr	Phe	Glu	Pro	Leu	Phe	Thr	Trp	Leu	Lys
216		585				590			595							
218	gac	cag	aac	aag	aat	tct	ttt	gtg	gga	tgg	agt	acc	gac	tgg	agt	cca
219	Asp	Gln	Asn	Lys	Asn	Ser	Phe	Val	Gly	Trp	Ser	Thr	Asp	Trp	Ser	Pro
220		600				605			610							
222	tat	gca	gac	caa	agc	atc	aaa	gtg	agg	ata	agc	cta	aaa	tca	gct	ctt
223	Tyr	Ala	Asp	Gln	Ser	Ile	Lys	Val	Arg	Ile	Ser	Leu	Lys	Ser	Ala	Leu
224		615				620			625							
226	gga	gat	aaa	gca	tat	gaa	tgg	aac	gac	aat	gaa	atg	tac	ctg	ttc	cga
227	Gly	Asp	Lys	Ala	Tyr	Glu	Trp	Asn	Asp	Asn	Glu	Met	Tyr	Leu	Phe	Arg
228		630				635			640							
230	tca	tct	gtt	gca	tat	gct	atg	agg	cag	tac	ttt	tta	aaa	gta	aaa	aat
231	Ser	Ser	Val	Ala	Tyr	Ala	Met	Arg	Gln	Tyr	Phe	Leu	Lys	Val	Lys	Asn
232	645					650			655			660				
234	cag	atg	att	ctt	ttt	ggg	gag	gag	gat	gtg	cga	gtg	gct	aat	ttg	aaa
235	Gln	Met	Ile	Leu	Phe	Gly	Glu	Glu	Asp	Val	Arg	Val	Ala	Asn	Leu	Lys
236		665				670			675							
238	cca	aga	atc	tcc	ttt	aat	ttc	ttt	gtc	act	gca	cct	aaa	aat	gtg	tct
239	Pro	Arg	Ile	Ser	Phe	Asn	Phe	Phe	Val	Thr	Ala	Pro	Lys	Asn	Val	Ser
240		680				685			690							
242	gat	atc	att	cct	aga	act	gaa	gtt	gaa	aag	gcc	atc	agg	atg	tcc	cgg
243	Asp	Ile	Ile	Pro	Arg	Thr	Glu	Val	Glu	Lys	Ala	Ile	Arg	Met	Ser	Arg
244		695				700			705							
246	agc	cgt	atc	aat	gat	gct	ttc	cgt	ctg	aat	gac	aac	agc	cta	gag	ttt
247	Ser	Arg	Ile	Asn	Asp	Ala	Phe	Arg	Leu	Asn	Asp	Asn	Ser	Leu	Glu	Phe
248		710				715			720							
250	ctg	ggg	ata	cag	cca	aca	ctt	gga	cct	cct	aac	cag	ccc	cct	gtt	tcc
251	Leu	Gly	Ile	Gln	Pro	Thr	Leu	Gly	Pro	Pro	Asn	Gln	Pro	Pro	Val	Ser
252	725					730			735			740				
254	ata	tgg	ctg	att	gtt	ttt	gga	gtt	gtg	atg	gga	gtg	ata	gtg	gtt	ggc
255	Ile	Trp	Leu	Ile	Val	Phe	Gly	Val	Val	Met	Gly	Val	Ile	Val	Val	Gly
256		745				750			755							
258	att	gtc	atc	ctg	atc	ttc	act	ggg	atc	aga	gat	cgg	aag	aag	aaa	aat
259	Ile	Val	Ile	Leu	Ile	Phe	Thr	Gly	Ile	Arg	Asp	Arg	Lys	Lys	Lys	Asn
260		760				765			770							
262	aaa	gca	aga	agt	gga	gaa	aat	cct	tat	gcc	tcc	atc	gat	att	agc	aaa
263	Lys	Ala	Arg	Ser	Gly	Glu	Asn	Pro	Tyr	Ala	Ser	Ile	Asp	Ile	Ser	Lys

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267	Gly	Glu	Asn	Asn	Pro	Gly	Phe	Gln	Asn	Thr	Asp	Asp	Val	Gln	Thr	Ser	
268	790					795							800				
270	ttt	tag	aaaaatctat	gttttcctc	ttgaggtat	tttgggttat	gtaaatgtta										2571
271	Phe																
272	805																
274	atttcatgg	atagaaaata	taagatgata	aagatatcat	taaatgtcaa	aactatgact											2631
276	ctgttcagaa	aaaaaaattgt	ccaaagacaa	catggccaag	gagagagcat	cttcatttgc											2691
278	attgtttca	gtatttattt	ctgtctctgg	atttgacttc	tgttctgttt	cttaataagg											2751
280	atttgtatt	agagtatatt	agggaaagtg	tgttatttgg	ctcacaggct	gttcagggat											2811
282	aatctaaatg	taaatgtctg	ttgaatttct	gaagttgaaa	acaaggatat	atcattggag											2871
284	caagtgttgg	atcttgtatg	gaatatggat	ggatcactt	taaggacagt	gcctggaaac											2931
286	tgggttagct	gcaaggattt	agaatggcat	gcattagctc	actttcattt	aatccattgt											2991
288	caaggatgac	atgctttctt	cacagtaact	cagttcaagt	actatggta	tttgcctaca											3051
290	gtgatgtttg	gaatcgatca	tgctttctt	aagggtacag	gtctaaagag	agaagaatcc											3111
292	agggAACAGG	tagaggacat	tgcttttca	cttccaaggt	gcttgcataa	catctccctg											3171
294	acaacacaaa	actagagcca	ggggcctccg	tgaactccca	gagcatgcct	gatagaaact											3231
296	catttctact	gttctcta	tgtggagtat	atggaaattt	caactgtatg	ttcaccctct											3291
298	gaagtggta	cccagtctt	taaatcttt	gtatttgc	acagtgttt	agcagtgc											3351
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345	<213>	ORGANISM:	Artificial Sequence														

VERIFICATION SUMMARY

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:10 M:270 C: Current Application Number differs, Replaced Current Application No

:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date